

Supporting Online Material for

An Epigenetic Role for Maternally Inherited piRNAs in Transposon Silencing

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Supplemental Materials and Methods

Fly stocks, maintenance and fertility analysis

The wildtype strains for the I-R hybrid dysgenesis system (inducer: w^{1118} ; reactive: w^k) were a kind gift of Silke Jensen and were originally described in (S1) and (S2). The wildtype strains for the P-M hybrid dysgenesis system (*Harwich* is a P-strain, which contains mobile, but repressed *P-elements* (S3); *Larik-P(1A)* is a P-strain, which contains two *P-elements* inserted into the X-TAS piRNA cluster of the X-chromosome (S4); *Nasr'Allah-P(1A)* is a P-strain, which contains one truncated and immobile *P-element* inserted into the X-TAS piRNA cluster of the X-chromosome (S5) were kindly provided by Stéphane Ronsseray. Flies were maintained at 22°C on standard medium. Reciprocal intercrosses were between 40 virgins and 10 males from the respective stocks, with all animals incubated at 22°C. Fertility of the parental strains and the reciprocal F1 daughters mated to their F1 brothers was determined by allowing caged flies to lay eggs for 24 hours onto grape-agar plates. Hatched eggs were counted 48 hours later.

Small RNA libraries

Total RNA was extracted using Trizol (Invitrogen) from dissected ovaries from 3-5 day old yeast-fed flies. Total RNA was extracted from 0-2h old dechorionated embryos laid by the respective strains at 22°C. Small RNAs from total RNA were cloned by ligation of 3' and 5' linkers, reverse transcription, and PCR amplification (detailed protocol available upon request). The following small RNA libraries from total RNA were prepared for this study: 18-29nt from ovaries and 0-2h embryos of the w^{1118} , w^k , *Harwich*, *Larik-P(1A)*, *Nasr'Allah-P(1A)*, strains; 18-29nt from ovaries of dysgenic F1 progeny (w^{1118} males crossed to w^k virgins for the I-R system; *Harwich* males crossed to w^{1118} virgins for the P-M system) and non-dysgenic (w^k males crossed to w^{1118} virgins for the I-R system; *Harwich* males crossed to *Larik-P(1A)* virgins and *Harwich* males crossed to *Nasr'Allah-P(1A)* virgins for the P-M system).

Libraries (4-5 million reads per library) were sequenced using the Illumina platform. Published libraries used in this study were Piwi/Aub/AGO3 immunoprecipitate libraries from ovaries (S6).

Bioinformatic analysis of small RNA libraries

The 36nt long Illumina reads were stripped of the 3' linker and the resulting small RNA sequences were mapped to the Release 5 genome sequence excluding the Uextra portion (S7, S8). Except for the *P-element* analysis, only reads matching the fly genome 100% were used for further analysis (see Table S1). For annotation, we used Flybase for protein coding genes, UCSC for non-coding RNAs and transposons/repeats (repeat masker tracks) and the most recent miRNA catalog (S9, S10). To control for sequencing depth, small RNA counts were normalized to 1 million small RNAs after subtracting those matching abundant cellular RNAs such as rRNAs, tRNAs and snoRNAs (Table S1). For the piRNA analysis, we selected small RNAs, which

exceeded 22 nt in length and were not annotated as miRNA, tRNA, rRNA, snoRNA, snRNA or smRNA.

For the transposon analysis, small RNAs > 22nt were mapped onto the Repbase collection (S11) of transposons with up to 3 mismatches (Table S2). Read counts of small RNAs mapping multiple times to one element were corrected by their mapping number. Only true transposons within Repbase were considered and Satellite or other types of repeats were excluded (Table S2). For the *P*-element analysis, small RNAs (23-29nt) from those RNAs NOT matching the release 5 genome were considered as the reference genome is an M-strain, lacking *P*-element sequences. The *P*-element sequence is not present in the repbase collection and was obtained from the Ashburner collection at BDGP (www.fruitfly.org/p_disrupt/TE.html).

Small RNA size profiles

After subtracting reads matching to rRNAs, tRNAs, snoRNAs, snRNAs and smRNAs, the remaining small RNAs were split into annotated microRNAs and remainder. As illustrated in (S12), the remainder can be split into AGO2 bound endogenous siRNAs (21nt) and piRNAs bound to Piwi, Aub and AGO3 (23-29nt). In the present study, only small RNAs corresponding to the piRNA population (23-29nt) were considered.

Immunofluorescence

Ovaries were dissected from 3-5 day old progeny of *w¹¹¹⁸* and *w^k* reciprocal crosses. Flies were reared and caged at 22°C and fed yeast paste on grape-agar plates for two days prior to dissection. *I*-element ORF-1 antibody was used at a 1:1000 dilution and immunostaining was performed as previously described in (S6).

For embryo staining, *w¹¹¹⁸* flies were caged and fed yeast paste. Embryos (0-20h) were collected, dechorionated in 50% bleach, fixed for 25min in the heptane/4%formaldehyde interface, devitellinized by rigorously shaking with methanol, and washed in PBS with 0.1% Tween-20. Primary antibodies were rabbit polyclonal sera purified against Piwi, Aub and AGO3 N-terminal peptides (S6). These were used at 1:750 dilutions. Alexa 488 secondary antibodies (Molecular Probes) were used at 1:800 and DNA was stained with DAPI. Images are confocal sections.

Analysis of active and heterochromatic *I*-fragments

The *I*-element sequence used for the active transposon was the Repbase entry I_DM (S11). Nucleotides 1-99 and 5471-6231 were removed, as those are *D. melanogaster* genomic sequences mis-annotated as *I*-element portions. For the detailed piRNA distribution analysis on this sequence, all piRNAs, which were annotated as I_DM derived from the repeatmasker tracks at UCSC, were extracted and mapped onto the active sequence allowing up to 5 mismatches, indels or bulges. For the piRNA density plots, piRNAs were collapsed to their 5' ends. Ping-pong partners were those sequences whose ten 5' nucleotides were reverse complements.

The population of annotated *I*-elements in the reference genome clearly splits into several elements with no or very few mismatches to the I_DM sequence (those classify as recent full length or truncated insertions of the active *I-element*) and numerous fragments, which exhibit 5% or more deviation (see Table S3). Genomic positions of all annotated *I*-fragments and their respective start and stop in the I_DM reference sequence were extracted from UCSC. *I-element* annotated piRNAs, which map the genome uniquely, were mapped to all identified fragments and the density was calculated as the number of unique mappers divided by the fragment length.

Ping-pong signature

We first matched all piRNA sequences to the Repbase transposon sequences, allowing for plus and minus strand matches with up to 3 mismatches, indels or bulges. Each piRNA was reduced to its 5'end. For each matched piRNA ("target piRNA"), we computed a histogram of distances/offsets to "partner" piRNAs that match to the opposite strand, for which each partner piRNA contributes its cloning/sequencing count, normalized to 100% over all partner piRNAs up to a distance of 25nt (note that each piRNA is a "partner" piRNA for all other piRNAs and also a "target" piRNA itself with all other piRNAs as "partners"). We then combined these histograms for each distance/offset by summing the values for that distance over all histograms, but weighting each histogram's contribution by the relative cloning/sequencing of the respective target piRNA for which the histogram was computed.

42AB piRNA cluster sequencing

Genomic DNA was isolated from ~15 adult female flies from both the *w*¹¹¹⁸ and *w*^k strains. 500ng of genomic DNA and long range Taq polymerase (ROCHE) was used to amplify ancestral *I-element* containing regions of the 42AB piRNA using the following primers, which prime outside the annotated *I*-fragments and thus increased the confidence that the correct regions were amplified.

*w*¹¹¹⁸:

42AB-1-F	ACGTCTCCCTTCCAGATCTCC
42AB-1-R	TAAGAAGGACACAAAGGGGGCTTC
42AB-2-F	ACGTCTCCCTTCCAGATCTCC
42AB-2-R	TAGCCACCAGAGGCCCTTCTATG
42AB-3-F	CGCGAAAACTAATTCACTTAATCC
42AB-3-R	CACATTAAGTCCTGAAAGTCTACACG

w^k:

42AB-1-F	ACGTCTCCCTTCCAGATCTCC
42AB-3-R	CACATTAAGTCCTGAAAGTCTACACG

Amplified PCR products were cloned into the TOPO pCR2.1 (INVITROGEN) vector and were sequenced using the following primers, staggered over the 42AB piRNA cluster genomic region:

M13 Forward (-20)	GTAAAACGACGGCCAG
M13 Reverse	CAGGAAACAGCTATGAC
42AB-2-F-1*	AACTGGACCAGCCGAAACAAACCTT
42AB-2-F-2	GGGAAGTCTTGAAGCCCCTTTG
42AB-2-F-3	GCGCGAAGAAAGTAGCCAGTAGTGC
42AB-2-F-4	TGAATCCCCTGGGCTTCCATAATC
42AB-2-F-5	CTTCGCTTCGACTCCGGTATTGG
42AB-2-F-6	TGCAAAATCGATGTACCCCTGGTGA
42AB-2-R-1*	CGCACCTGACAAAGTGGATTAAGTGA
42AB-2-R-2	GTTTCTCTCGAGCCCCAATGTG
42AB-2-R-3	ACAGGCCTTACAGGGTATGCGTGA
42AB-2-R-4	CCAGAACGTGGAGTGGCTGGAAGAA
42AB-2-R-5	GCGTATCCACGAAGTTGCCTGAAG
42AB-2-R-6	GCTGGGCATCCACGCTAACATAAG
42AB-3-F-1*	CCAAAAAACACACCAATTACAAGTCG
42AB-3-F-2*	ACATCTCGGCTTGGGTTCTGTT
42AB-3-F-3*	ATCATTGTCCTGACCCCACGTCTC
42AB-3-F-4*	TTACCCAAAACAATCCCACGCAAA
42AB-3-R-1*	GCCCACACTGATTGCTAGGGACT
42AB-3-R-2*	TTTGTCGCACGATGGCTTAAG
42AB-3-R-3*	TCACCGCATCAAACACAGTTCAC
42AB-3-R-4*	ACCCACTGCTTCAGTCGCCTCTAA

* used to sequence the *w^k* strain genomic region.

Supplementary Figures

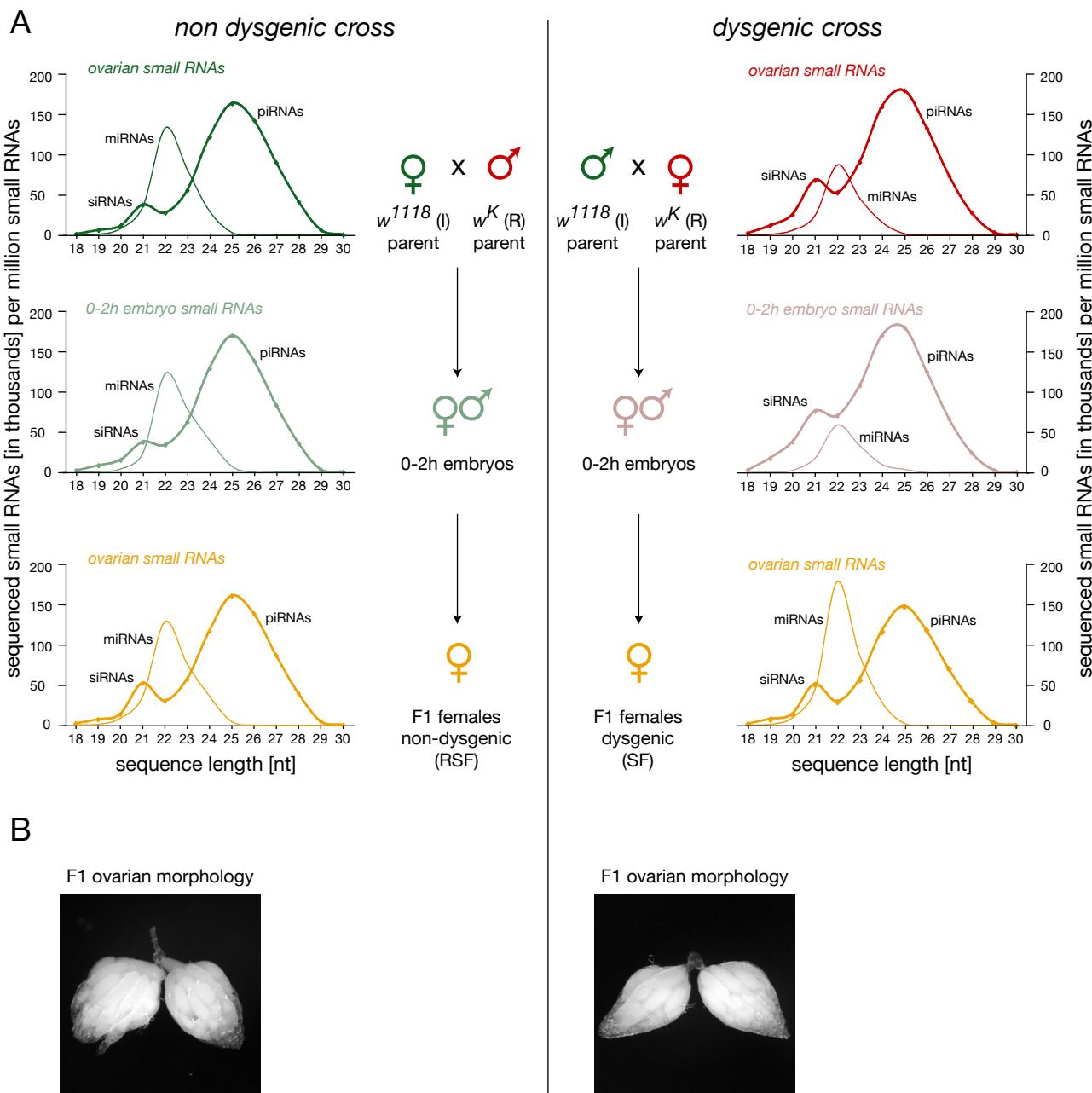


FIGURE S1

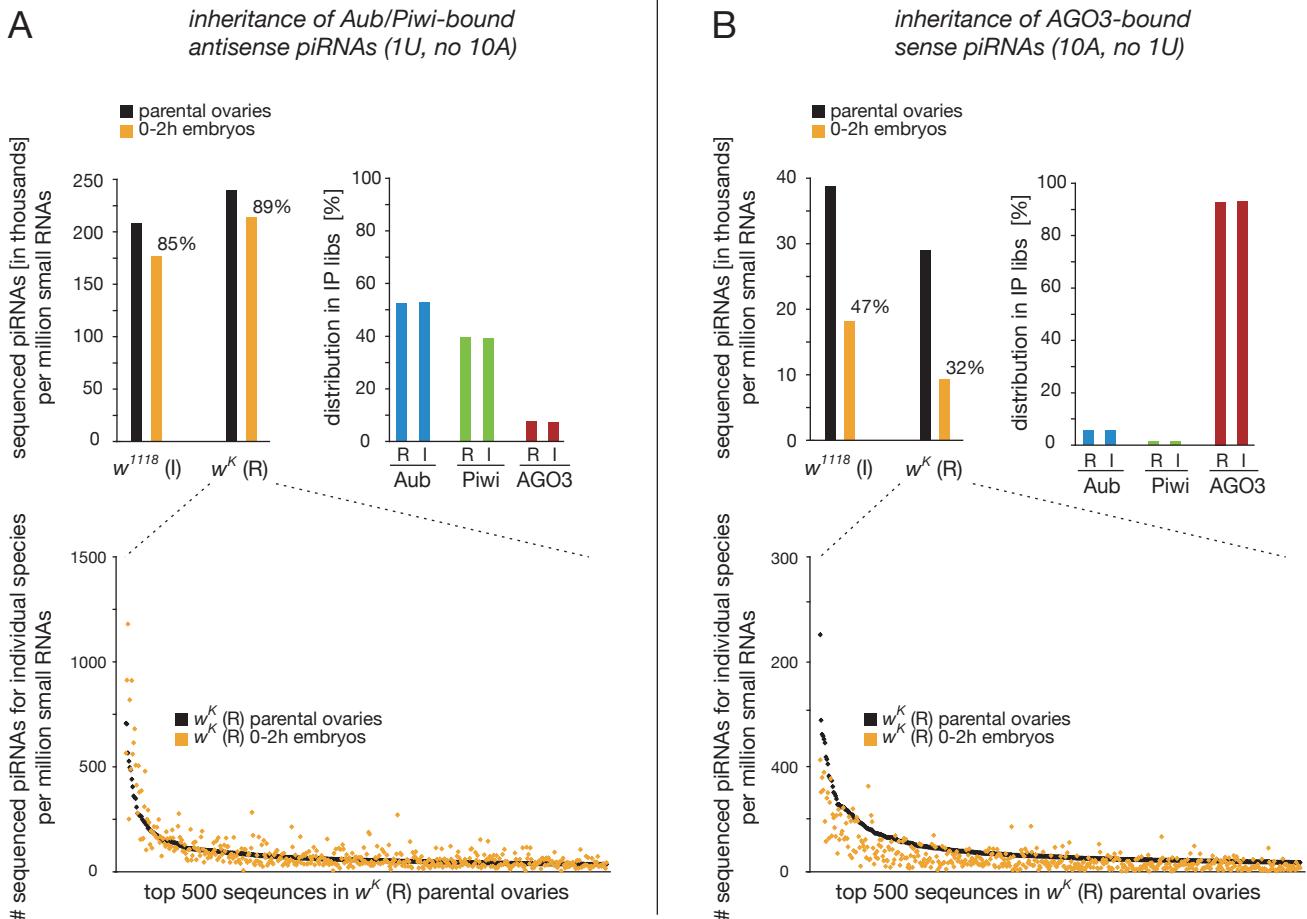


FIGURE S2

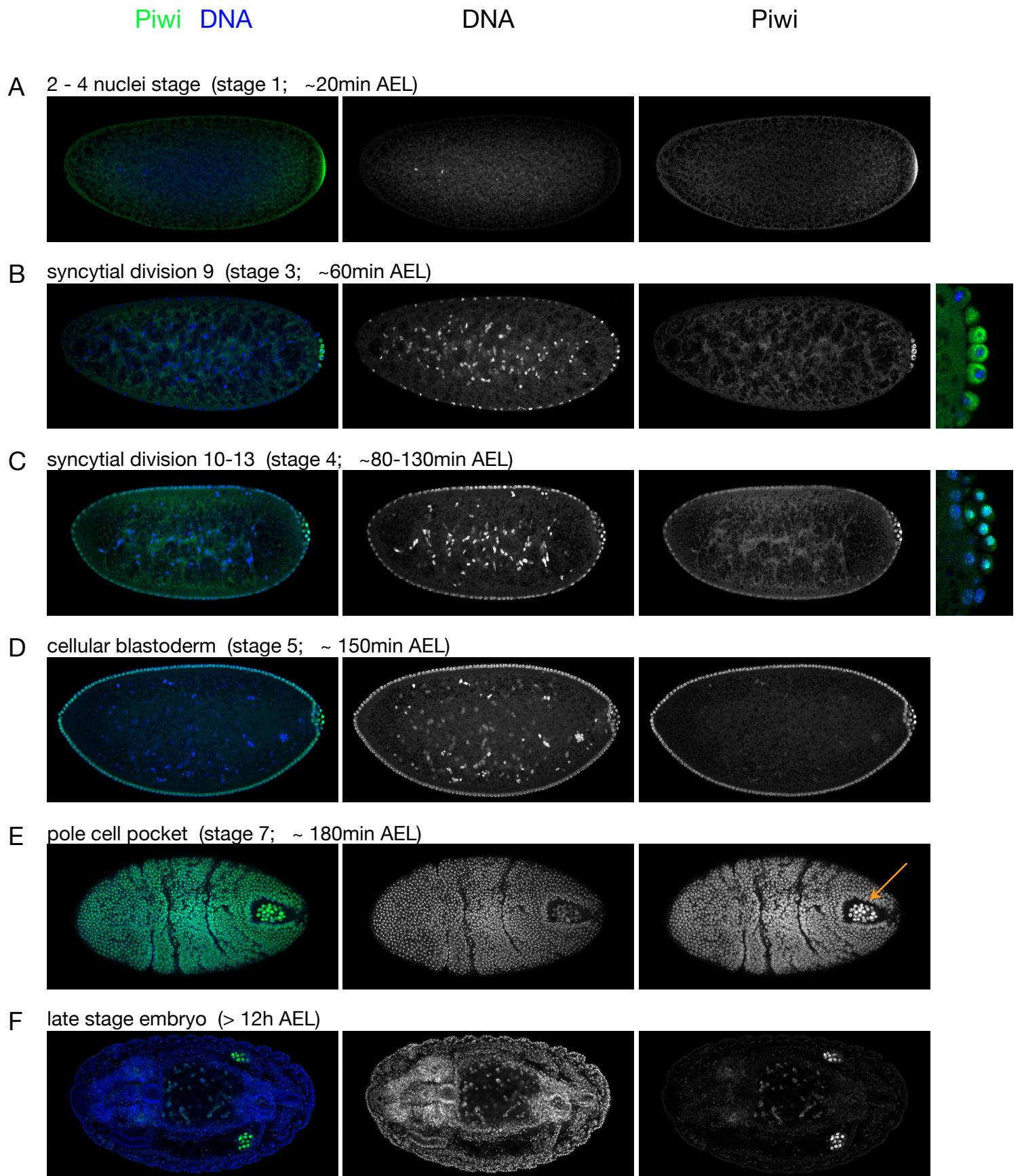


FIGURE S3

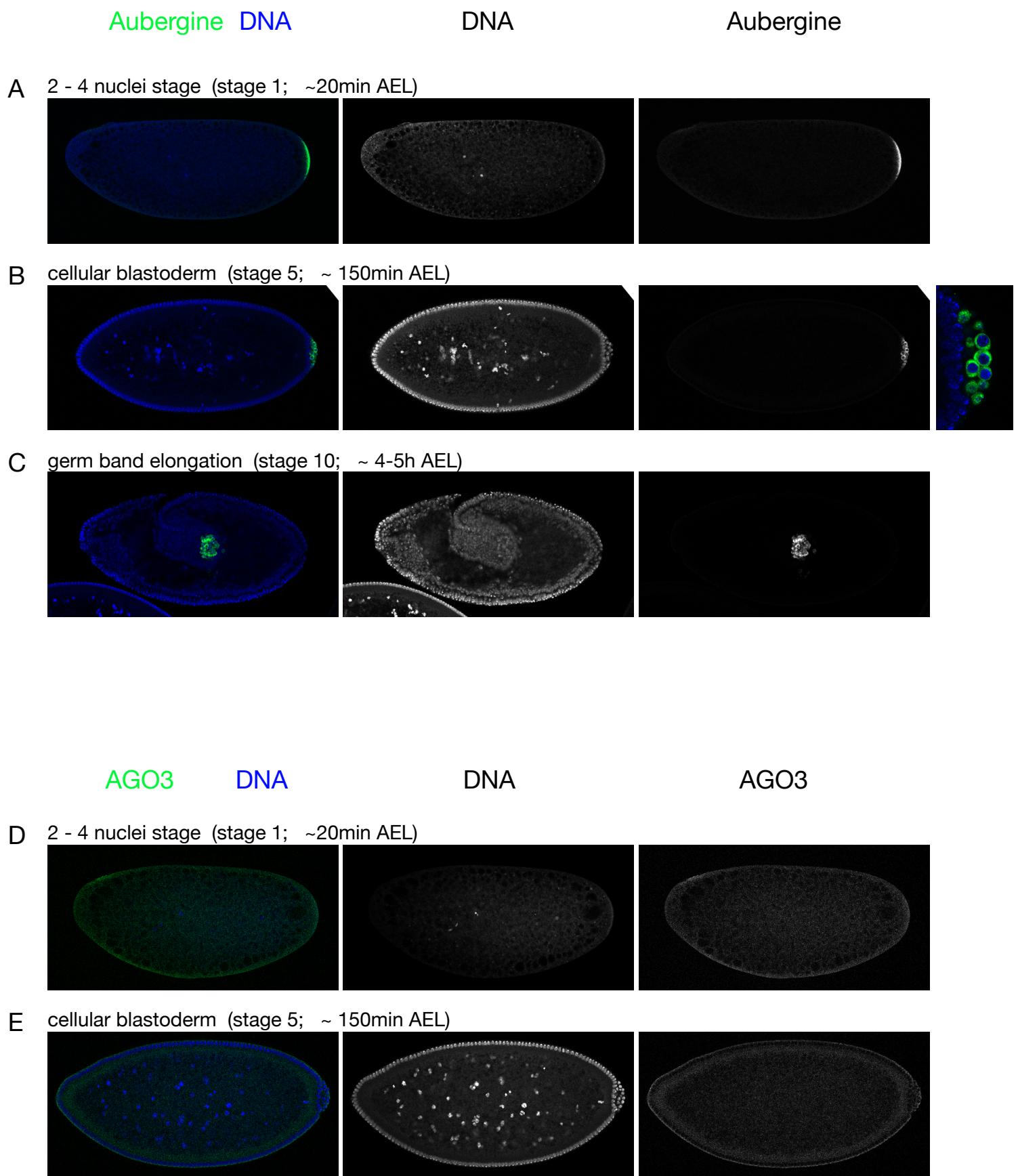
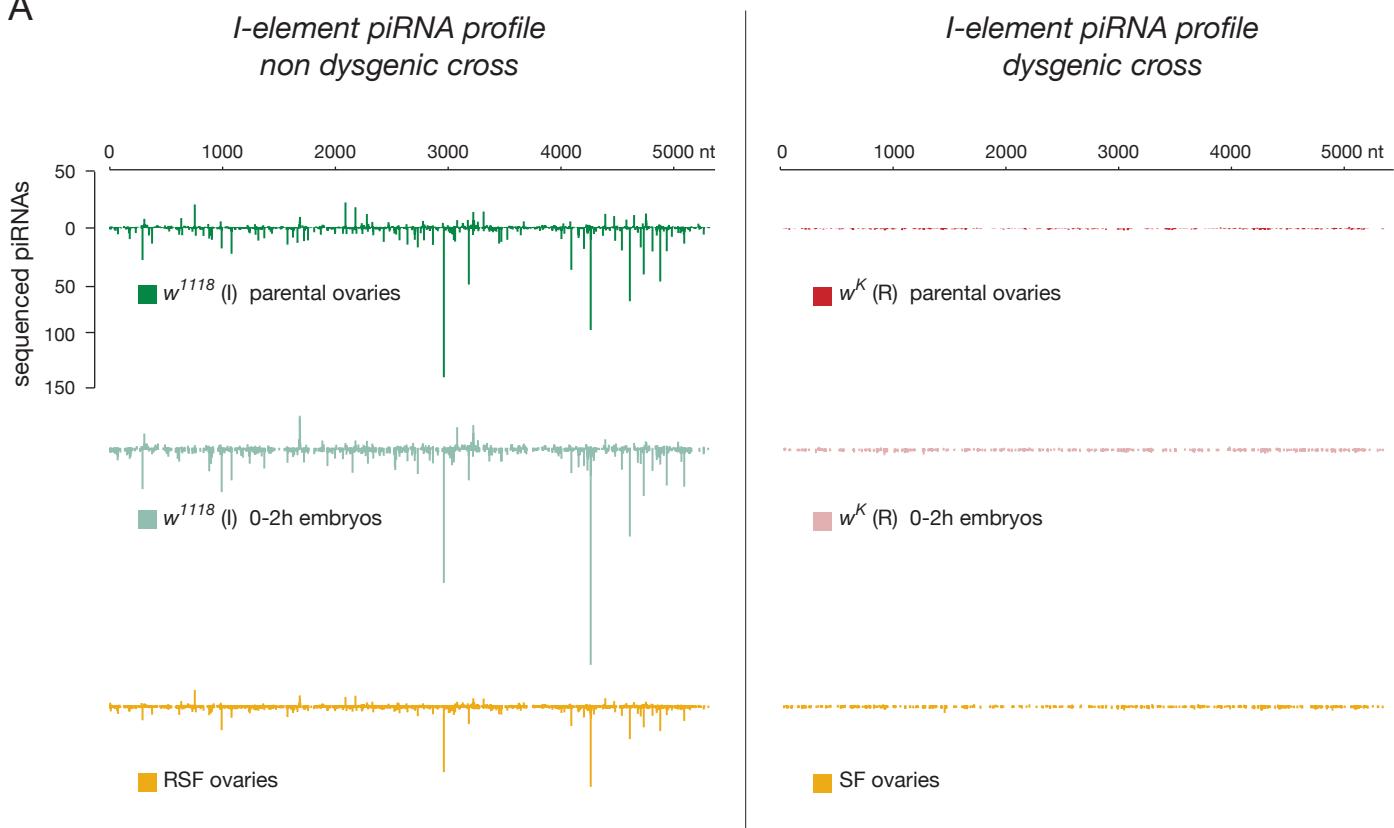


FIGURE S4

A



B

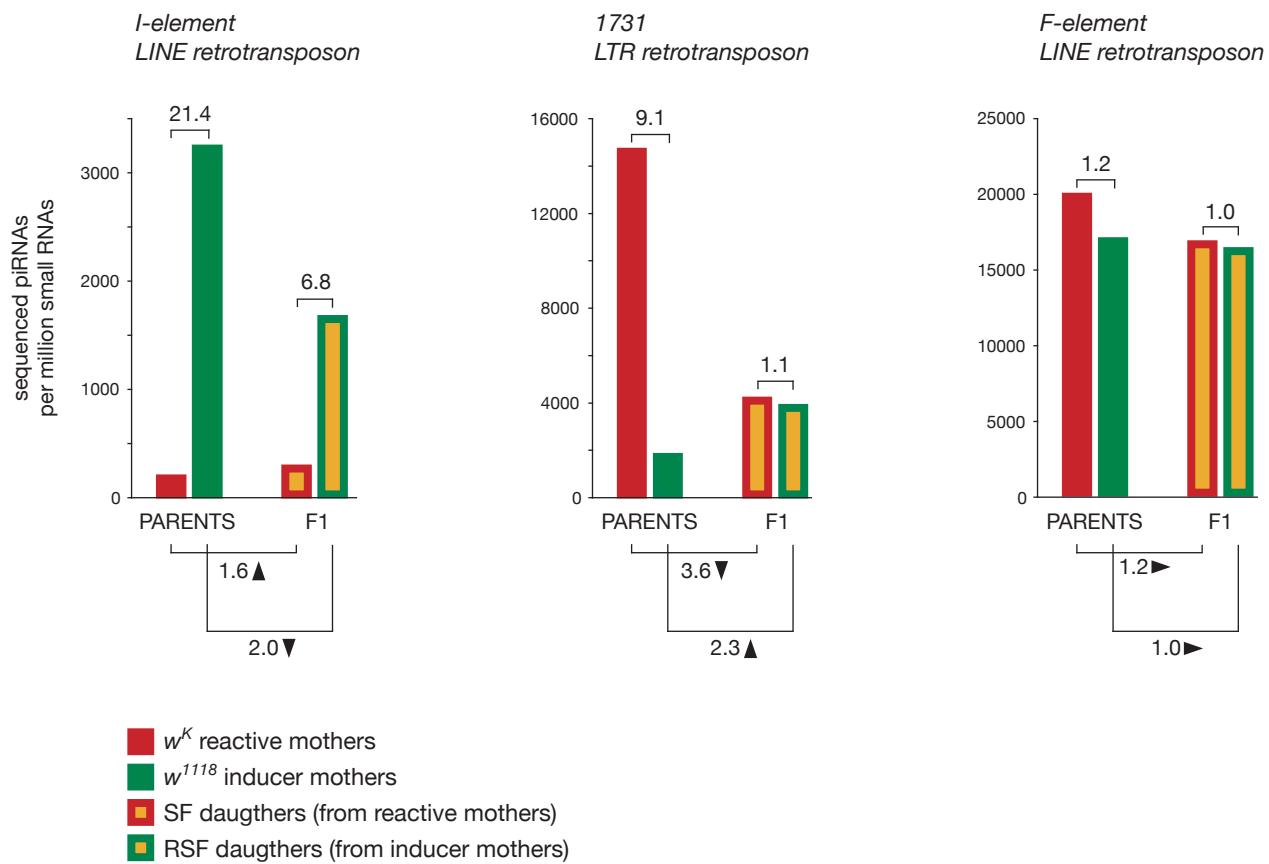
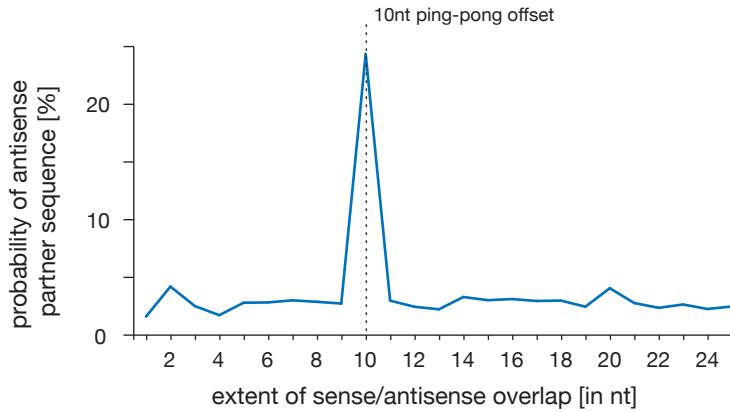
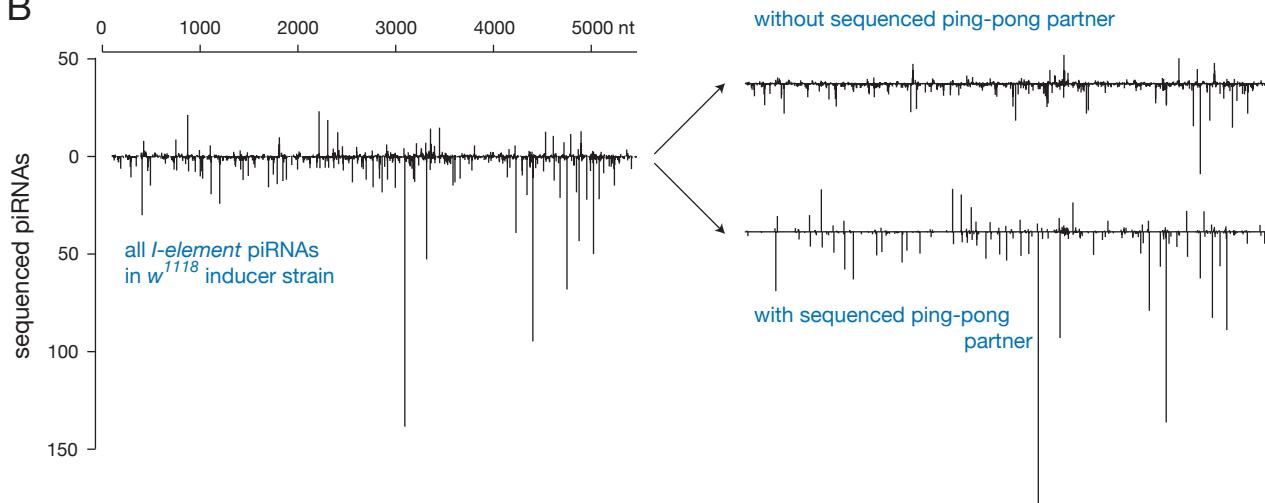


FIGURE S5

A



B



C

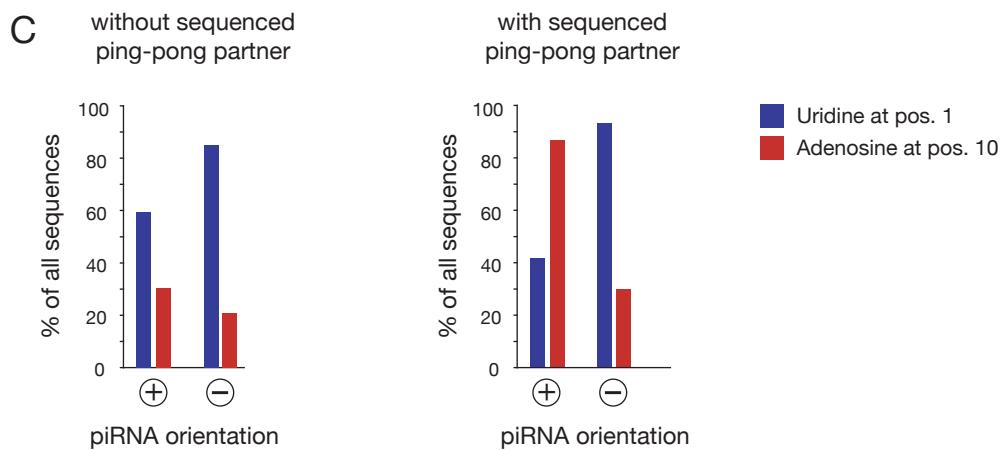


FIGURE S6

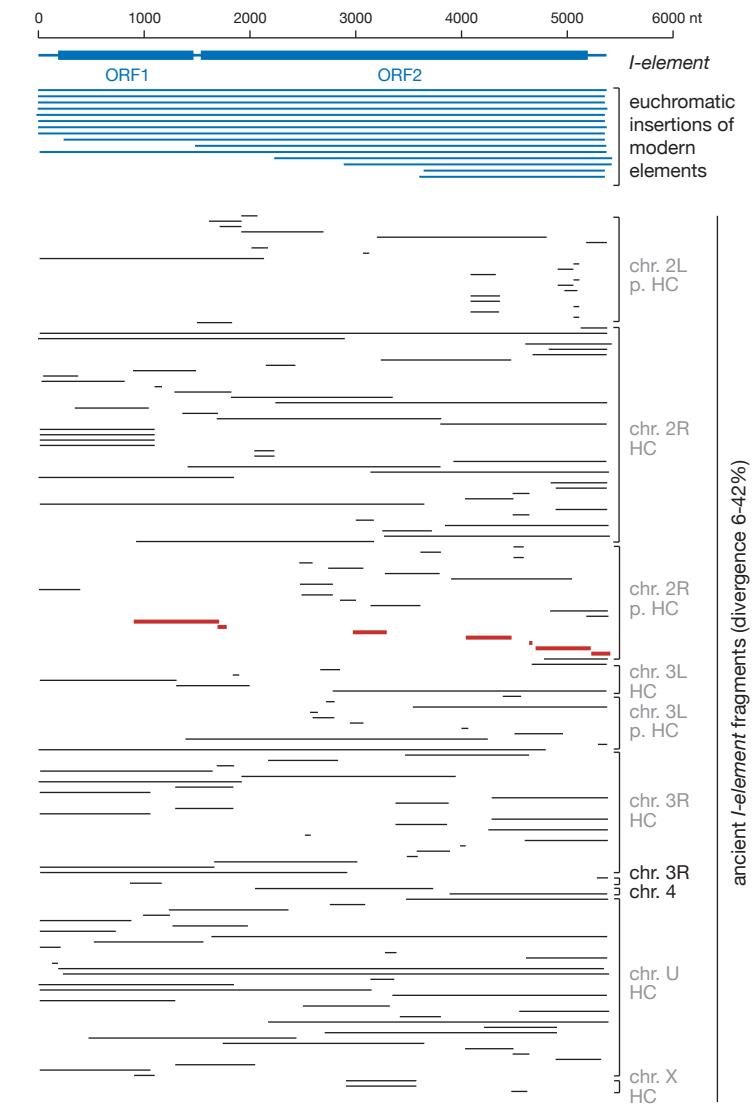
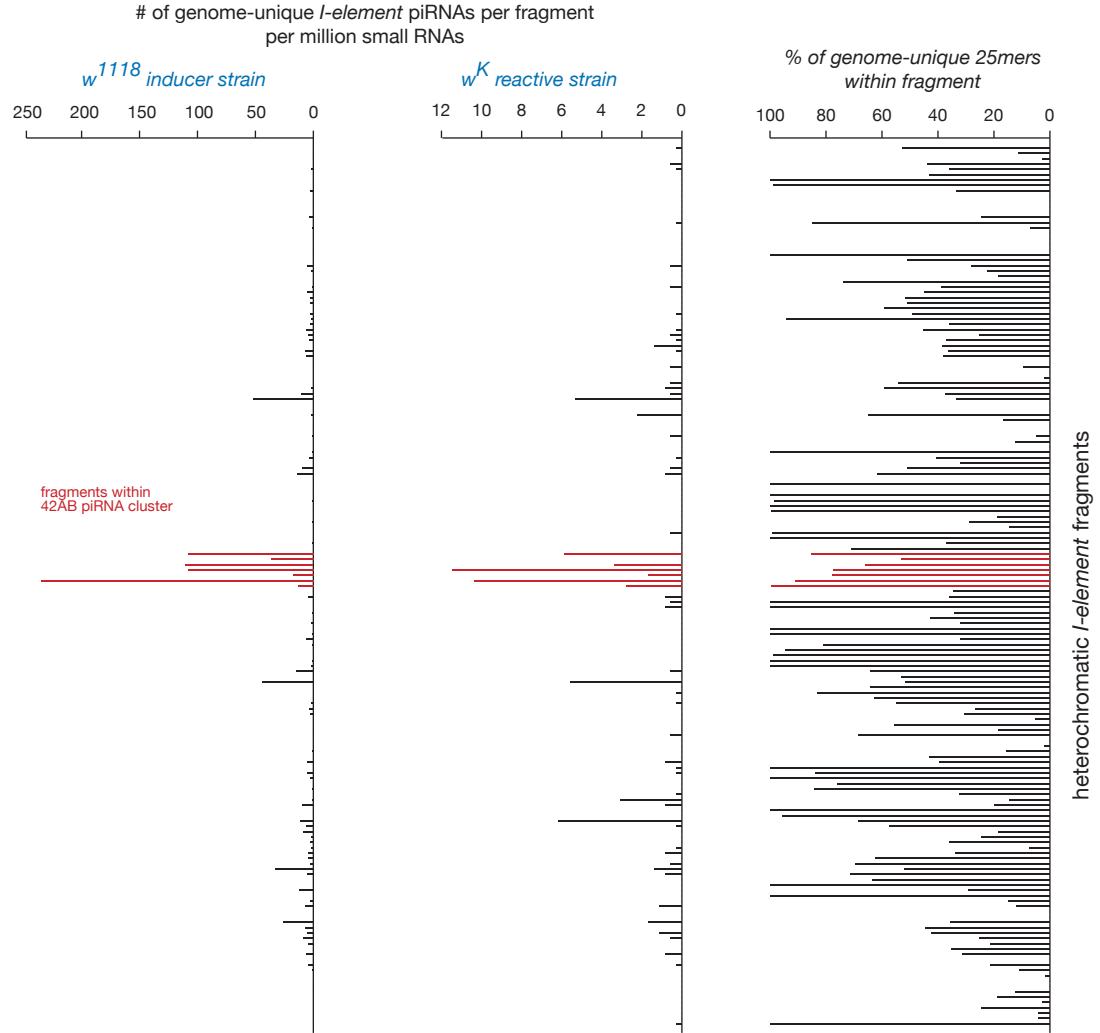


FIGURE S7

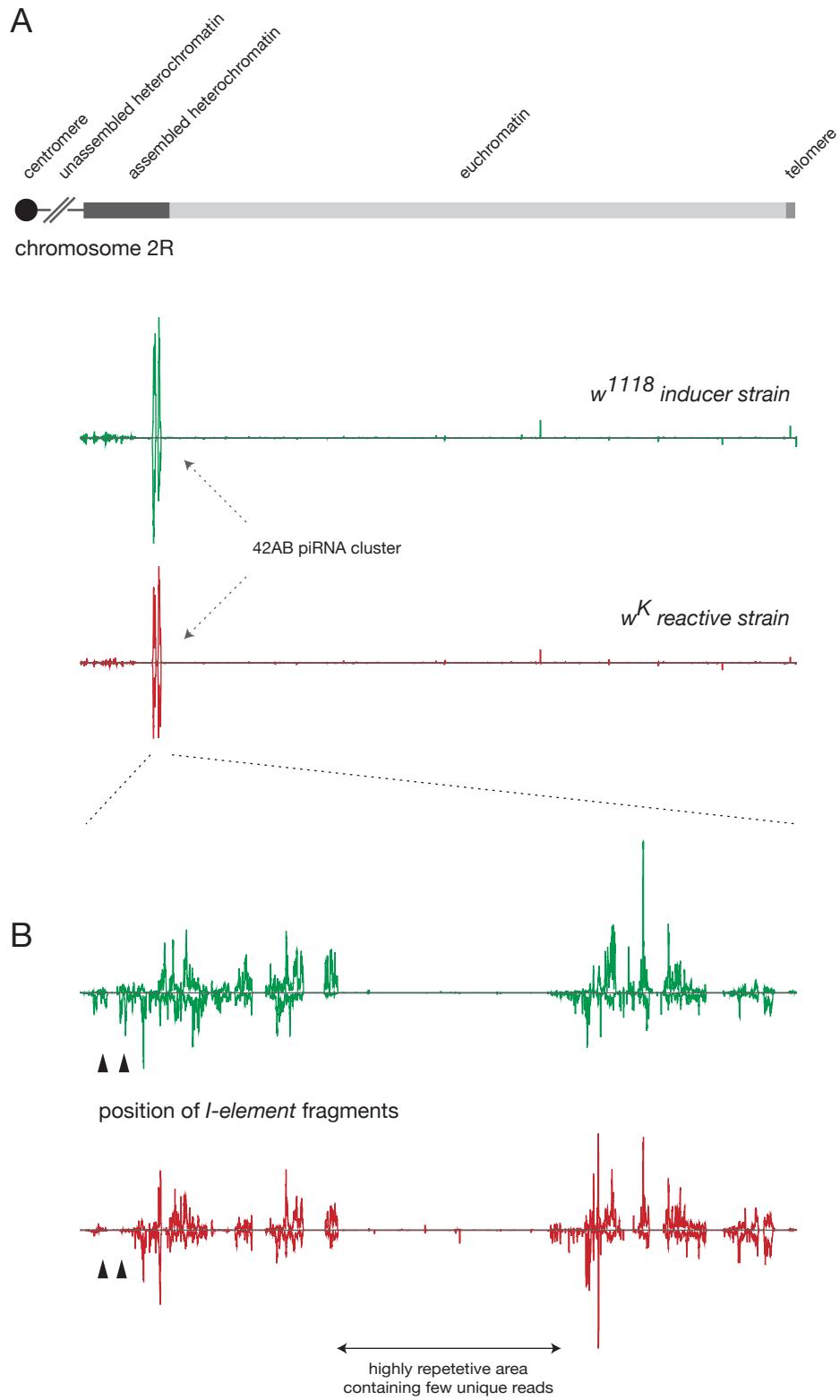


FIGURE S8

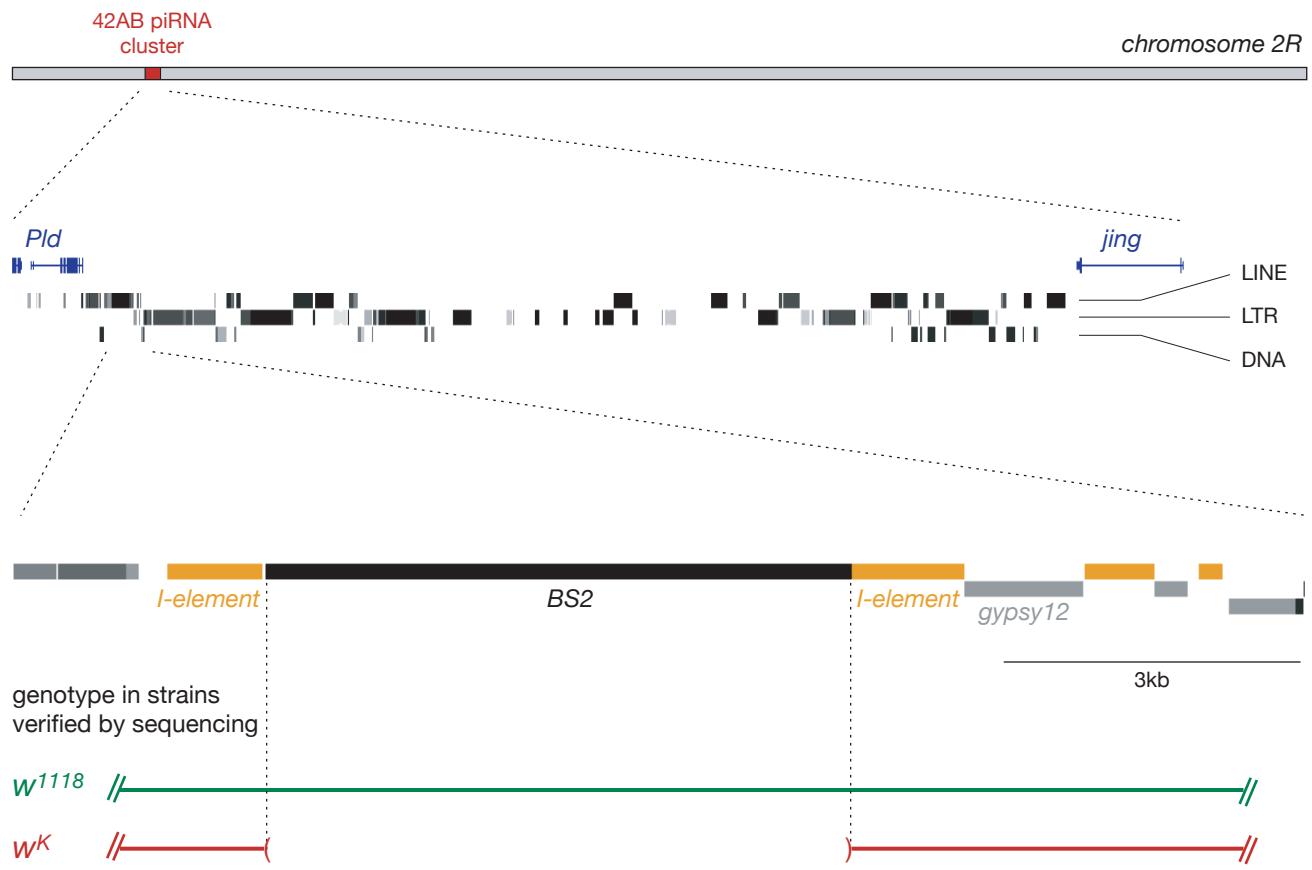


FIGURE S9

Supplementary Figure Legends

Figure S1. Crossing scheme and size profiles of sequenced small RNAs in the I-R Hybrid dysgenesis system.

(A) Small RNA profiles obtained from total RNA from maternal ovaries, early embryos (0-2h), and F1 ovaries derived from non-dysgenic and dysgenic intercrosses between w^{1118} inducer flies and w^k reactive strains. Size profiles show all small RNAs except those annotated as abundant non-coding cellular RNAs such as rRNAs, tRNAs and snoRNAs (levels are normalized to 1 million sequenced *bona fide* small RNAs). microRNAs were defined by annotation, siRNAs (21nt) and piRNAs (23-29nt) were defined by their characteristic size profiles. For unknown reasons, w^k mothers and their eggs showed a relatively lower ratio of piRNAs to miRNAs compared to w^{1118} . (B) Morphology of dysgenic and non-dysgenic ovaries.

Figure S2. Maternal inheritance of piRNA populations

(A) Inheritance of Piwi and Aub bound piRNAs: To the left, levels of piRNAs antisense to annotated transposons, which display a Uridine at position 1 (characteristic for Piwi and Aub bound piRNAs) and no Adenosine at position 10 (characteristic for AGO3 bound piRNAs) are shown for parental ovaries (black) and 0-2h embryos (orange) from the w^{1118} and the w^k strains. Note that the embryonic count corresponds to the level of all piRNAs, which were identified in the respective ovary library (piRNAs only sequenced in the embryonic library were not considered). To the right, recovery of the indicated piRNA pool in libraries from Piwi, Aub and AGO3 immuno-precipitates is shown. Below, the individual counts of the 500 most abundant ovarian piRNAs from the reactive w^k strain are shown, indicating highly consistent inheritance. (B) As in (A) but after selecting piRNAs, which are sense to annotated transposons and have an Adenosine at position 10 but no Uridine at position 1 (AGO3 pool of piRNAs). The degree of inheritance is significantly lower than that observed in (A).

Figure S3. Piwi localization and expression during embryogenesis

Piwi protein (green) and DNA (blue) are shown at characteristic stages of embryogenesis (A-F; embryonic stages and minutes of development after egg laying (AEL) indicated to the left). All images are anterior to the left and dorsal up unless otherwise indicated. (A) Maternally inherited Piwi is concentrated at the posterior pole right after egg laying (germ plasm). (B) During pole cell formation, Piwi protein localizes to the cytoplasm of pole cells (see small panel to the right). (C) During the last syncytial division, Piwi translocates to the nuclei of both pole cells (see also small panel to the right) and somatic cells. (D) At the cellular blastoderm stage, Piwi localizes uniformly to pole cell and somatic nuclei. (E) At the beginning of germ band extension, germ cells reside in a pocket and stain strongly for nuclear Piwi (dorsal view; anterior left). (F) In late stage embryos,

Piwi is predominantly detected in germ cell nuclei, while its somatic staining fades (dorsal view; anterior left).

Figure S4. Aubergine and AGO3 localization and expression during embryogenesis

Aub protein (green; upper three rows), AGO3 protein (green; lower two rows) and DNA (blue) are shown for characteristic stages of embryogenesis (A-E; embryonic stages and minutes of development after egg laying (AEL) indicated to the left). All images are anterior to the left and dorsal up unless otherwise indicated. **(A)** Maternally inherited Aub is strongly concentrated at the posterior pole right after egg laying (germ plasm). **(B)** At the cellular blastoderm stage, strong Aub staining is detected in the pole cell cytoplasm. **(C)** During germ band elongation, primordial germ cells localize dorsally to the midgut and strongly stain for Aub. **(D, E)** No specific localization or strong deposition of AGO3 is detectable shortly after egg laying (D) or at cellularization (E) or later embryonic stages (not shown). Note that ovaries stained in parallel under identical conditions exhibit strong AGO3 staining in the germline.

Figure S5. Lack of maternally inherited piRNAs prevents buildup of a piRNA response in F1 females.

(A) Indicated are normalized densities of piRNAs matching the *I-element* with up to five mismatches in maternal, embryonic, and SF and RSF F1 females of reciprocal crosses between inducer and reactive strains. Note that females of the two F1 generations are identical in their genotype (transposon load and piRNA clusters). **(B)** piRNA levels are shown for reactive (red) and inducer (green) mothers and for their respective RSF and SF F1 progeny (yellow; boxing indicates identity of maternal strain). Shown are values for three different transposons: For the *I-element*, no equilibrium is reached in the SF progeny, while non-dysgenic, RSF progeny show equilibration of piRNA levels corresponding to the reduced number of active elements compared to the *w¹¹¹⁸* strain. The 1731 element exhibits a strong difference between maternal strains but reaches equilibrium in the F1 generations (note that the relative number of piRNAs as compared to the *I-element* is about 10-fold higher). The *F-element* shows comparable piRNA levels in the two parental strains and accordingly little or no change in the F1 generations.

Figure S6. *I-element* specific piRNAs exhibit a ping-pong signature

(A) The graph indicates the probability of an existing antisense piRNA starting at the indicated distance in nt (for each piRNA, only the 5' end is considered) as calculated for a randomly chosen piRNA from the *w¹¹¹⁸* inducer strain. **(B)** Shown are density profiles of piRNAs matching the *I-element* with up to five mismatches (left) and respective profiles for those species with no identified ping-pong partner (right top) and those with an identified ping-pong partner (right bottom). Note that piRNAs involved in the ping-pong cycle are considerably more abundant than those with no identified ping-pong partner. **(C)** Further indication of two distinct populations of *I-element* piRNAs can be inferred from the

nucleotide composition of ping-pong piRNAs and all others. Only ping-pong sense piRNAs exhibit the strong bias for adenosine at position 10, typical for AGO3 bound species (note that the background frequency for adenosine on the sense strand is ~40%, for uridine on the sense strand is ~20%).

Figure S7. Ancestral *I*-fragments in the 42AB piRNA cluster as major piRNA source.

Bar diagrams are similar to those shown in Fig.3, with the absolute number of piRNAs plotted per annotated ancestral *I-element* fragment in inducer and reactive strains (only piRNAs, which map uniquely to the release 5 genome were analyzed). The diagram in the center indicates the degree of sequence uniqueness of each annotated fragment. 25 nt windows were shifted across each fragment and the percentage of those 25mers which mapped exclusively to this fragment and nowhere else in the genome were determined. To the right, all genomic *I-element* fragments are shown as in (Fig. 3). *I*-fragments residing within the 42AB piRNA cluster are colored in red.

Figure S8. The 42AB cluster is a major source of piRNAs in inducer and reactive strains

(A) A cartoon of chromosome 2R (top) indicates the position of the centromere, un-assembled and assembled pericentromeric heterochromatin, euchromatin, and telomere. The green and red graphs below indicate the density of uniquely mapping piRNAs along the chromosome 2R sequence in inducer and reactive strains, respectively. The prominent piRNA cluster at 42AB in both strains is magnified in (B). Positions of annotated *I*-fragments are indicated by arrowheads (note the absence of piRNAs in these regions in the reactive strain). The central portion of 42AB is highly repetitive, negating the possibility of uniquely mapping piRNAs.

Figure S9. Ancestral *I*-fragments within the 42AB piRNA cluster are present in reactive and inducer strains

A cartoon depicts the largest known piRNA cluster in females, lying at cytological position 42AB. The top bar indicates the entire right arm of chromosome 2 with the centromere to the left and the telomere to the right. Below, flanking protein coding genes (blue) and transposons (LTR elements, LINE elements, DNA elements) are indicated as annotated by the repeat masker tracks of the UCSC genome browser. Below, ~12kb of the beginning of the 42AB cluster are magnified and annotated ancestral *I*-fragments are colored in yellow. The green and red lines at the bottom indicate the architecture of the 42AB cluster in the reactive (red) and inducer (green) strain. Note that all *I*-fragments were unambiguously identified in both strains. The BS2 insertion present in the Celera sequencing strain (Release 5 of the *D. melanogaster* genome) is found only in the inducer strain, indicating a recent insertion of this full-length element.

Supplementary Tables

Table S1. Normalization of P-element libraries

	wK_parental_ovaries	wK_0-2h_embryos	wK_F1_ovaries	w1118_parental_ovaries	w1118_0-2h_embryos	w1118_F1_ovaries	NA_parental_ovaries	NA_0-2h_embryos	NAxHar_F1_ovaries	LK_parental_ovaries	LK_0-2h_embryos	LKxHar_F1_ovaries	Har_parental_ovaries	Har_0-2h_embryos	w1118xHar_F1_ovaries
all reads	4988425	5434920	5223749	524374	5224324	4315260	5316812	5625880	6647804	5251511	5846541	6391886	6365113	6702532	6590352
not mapping to release 5	1201975	1343462	761356	806956	1031037	799788	1122707	1340674	1202555	1242476	1794969	1249487	1047936	1222912	1619240
mapping to release 5	3786450	4091458	4512393	4417418	4243337	3515472	4194105	4335206	5445246	4052665	4051572	5317177	5484620	4971112	
% of all reads mapped	~50	~73	~55	~65	~65	~55	~71.9	~71.4	~75.5	~75.5	~75.5	~75.5	~75.5	~75.5	~75.5
bona fide small RNAs*	3583376	3475887	4273771	4139901	3455533	3280435	3073787	3398772	4877226	3569134	2973266	4712337	2962527	2092078	3679418
% of mappers	94.6	85.0	94.7	93.7	81.4	93.3	73.3	78.4	89.6	88.1	73.4	91.6	55.7	38.1	74.0
miRNAs	646854	438936	1508704	1215911	966377	959168	1112718	953845	1760069	1382873	952451	1775424	897768	569065	2555631
% of mappers	17.1	10.7	33.4	27.5	22.8	27.3	26.5	22.0	32.3	34.1	32.5	34.1	16.9	10.4	31.4
% of bona fide small RNAs	18.1	12.6	32.3	29.4	28.0	29.2	36.2	28.1	36.1	38.7	32.0	37.7	20.3	27.2	69.5
P-element piRNAs (23-29nt)**	0	3	0	0	0	0	1846	2953	9754	2020	1891	11131	5862	2492	508
normalization factor ***	3.58	3.48	4.27	4.14	3.46	3.28	3.07	3.40	4.88	3.57	2.97	4.71	2.96	2.09	3.68

* after subtraction of RNAs annotated as rRNA, tRNA, snoRNA, snRNA, miRNA, mitochondrial

** note that the Celera reference genome is an M-strain; thus P-element piRNAs were extracted from the non-mappers by allowing up to 1 mismatch to the canonical P-element sequence

*** per 1 million bona fide small RNAs

Table S2. Total piRNA counts (normalized to 1Mio small RNA reads) per indicated Repbase transposon; up to 3MM between small RNA and indicated element were permitted (piRNAs mapping multiple times within one element were counted only once)

for Quasimodo2, Copia2, MDG3 and HMSBeagle, the internal and LTR parts (which are listed separately in Repbase) were fused; the following Repbase entries were excluded from the analysis as they either represent incomplete elements, no transposable ele-

the following Repbase entries were excluded from the analysis as they either represent incomplete elements, non-transposable elements or Satellite repeats

PEN1, PLACW_DM, PEN2, ALA_DM, DMDPR, DMRP1, DMSAT6, DMHMR1, NTS_DM, DMTO1M1_LTR, RSP, STALKER3_LTR, DMLTR5, LTRMDG3_DM, XDMR, HELENA_RT, GYPSY6A_LTR, GYPSY12A_LTR, DM412B_LTR, DMHMR2, ARS406_V1_DM, SAR_DM, TART_B1, HETR_DM

GTP5T18A_LTR, GTP5T12A_LTR, DM412B_LTR, DMHMR2, ARS406_DM, SAR_DM, TART_B1, HETRP_DM

element	family	position	wk_1_parental_ovaries	wk_0-2h_embryos	wk_F1_ovaries	w118_parental_ovaries	w118_0-2h_embryos	w118_F1_ovaries	average parent	w118_parent/wk_parent	log2 ratio	ratio factor	w118_embryo/wk_embryo	log2 ratio	ratio factor	w118_F1/wk_F1	log2 ratio	ratio factor		
ALUII_DM	SINE1	117	1	3	2	1	0	1	1	1.3	0.0	0.5	#DIV/0!							
Transib-N1_DM	He100	116	0	2	3	0	2	1	1	2.2	1.3	1.0								
TRANTRON1_DM	He100	114	1	1	2	3	5	2	2	5.2	0.6	1.0								
TLD1	Non-LTR	113	7	11	12	13	6	12	10	2.0	1.4	1.0								
MARINER2_DM	Mariner/Tc1	113	11	12	10	13	30	14	12	1.2	2.6	1.4								
Transib1	Transib	112	16	13	11	10	12	7	13	0.6	0.9	0.6								
TLD3	Non-LTR	111	7	7	13	25	9	15	16	3.5	1.2	1.1								
TC1_DM	Mariner/Tc1	110	21	26	24	34	36	25	27	1.6	1.4	1.0								
TLD2	Non-LTR	109	22	12	26	38	17	16	30	1.7	1.4	1.0								
BS4_DM	Jockey	108	29	46	37	50	47	53	40	1.7	1.0	1.4								
TRANSP1	Copia	107	58	69	33	25	23	23	41	0.4	0.3	0.7								
TRANS1B3	Transib	106	19	31	25	82	90	43	50	4.3	2.9	1.9								
INVADERS	Gypsy	105	91	119	44	40	45	41	66	0.4	0.4	0.9								
G3_DM	Jockey	104	73	111	88	102	106	79	88	1.4	1.0	0.9								
S2_DM	Mariner/Tc1	103	107	78	78	79	74	61	93	0.7	0.9	0.8								
G7_DM	Jockey	102	35	42	71	154	124	108	94	4.4	3.0	1.5								
GYPSY9	Gypsy	101	104	88	97	127	94	99	116	1.2	1.1	1.0								
P0GON1	Mariner/Tc1	100	260	248	148	154	134	160	207	0.6	0.5	1.1								
GYPSY10	Jockey	99	144	115	308	508	211	209	509	5.0	5.3	2.3								
Transib1	Transib	98	292	351	235	176	167	237	234	0.6	0.5	1.0								
R2_DM	R2	97	189	277	234	280	335	304	235	1.5	1.2	1.3								
FB4_DM	Mariner/Tc1	96	297	251	145	275	211	205	286	0.9	0.8	1.4								
G5_DM	Jockey	95	72	103	142	522	639	321	297	7.2	6.2	2.3								
Transib5	Transib	94	211	191	419	357	255	315	2.0	1.9	1.3									
DMRT1C	Non-LTR	93	162	289	292	509	704	462	336	3.1	2.4	1.6								
DOC4_DM	Jockey	92	381	334	297	364	315	373	1.0	1.3	1.1									
GYPSY11	Jockey	91	234	128	126	141	459	370	373	2.2	2.5	1.1								
JOCKEY2	Jockey	90	248	346	241	340	212	241	364	0.8	0.6	1.1								
TC1-2_DM	Mariner/Tc1	89	259	332	291	521	552	339	390	2.0	1.7	1.2								
LOOPER1_DM	piggyBac	88	392	492	266	389	266	363	391	1.0	0.5	1.4								
DOCS_DM	Jockey	87	350	381	393	546	618	433	448	1.6	1.6	1.1								
GYPSY12	Gypsy	86	506	496	421	423	432	383	464	0.8	-0.3	1.2	0.9	-0.2	1.1	0.9	-0.1	1.1		
TRANSPEC	Gypsy	85	504	334	373	454	342	365	479	0.9	-0.2	1.1	1.0	0.0	1.0	1.0	0.0	1.0		
FW3_DM	Jockey	84	638	584	514	499	515	568	0.8	-0.4	1.3	0.9	-0.2	1.1	0.9	-0.1	1.1			
GYPSY13	Gypsy	83	672	599	388	300	407	605	0.4	-1.4	2.8	1.1	0.0	-0.1	1.1	0.0	-0.1	1.1		
BARDL_DM	Mariner/Tc1	82	498	444	563	777	646	442	638	1.6	0.6	1.5	0.5	1.5	0.8	-0.3	1.8			
ZAM	Gypsy	81	595	75	606	753	293	661	674	1.3	0.3	1.3	3.9	2.0	1.1	0.1	1.1			
ACCORD2	Gypsy	80	1002	1025	643	370	393	606	686	0.4	-1.4	2.7	0.4	0.4	-1.4	2.6	0.9	-0.1	1.1	
GYPSY14	Gypsy	79	595	716	975	1238	1529	1246	917	2.1	1.1	2.1	2.1	1.1	2.1	1.3	0.4	1.3		
FW2_DM	Jockey	78	1045	1122	811	809	1353	986	927	0.8	-0.4	1.3	1.2	0.3	0.8	1.2	0.3	0.8		
M4DM	DNA	77	1394	1253	591	629	435	526	1011	0.5	-1.1	2.2	0.3	-1.5	2.9	0.9	-0.2	1.1		
R1-2_DM	Non-LTR	76	1228	1307	945	837	789	1244	1033	0.7	-0.6	1.5	0.7	-0.5	1.5	1.2	0.2	1.2		
ACCORD3	Gypsy	75	1257	1294	794	555	872	1099	555	0.5	-0.9	1.8	0.5	-0.5	1.5	1.2	0.3	1.2		
BSS_DM	Jockey	74	915	1060	1182	1340	1751	1498	1127	1.5	0.5	1.1	1.7	0.7	1.7	1.3	0.3	1.3		
G4_DM	Jockey	73	1371	1561	1183	1214	1113	1199	1293	0.9	-0.2	1.1	1.1	0.7	-0.5	1.4	1.0	0.0	1.0	
HOB0	hAT	72	1333	1268	977	1259	1229	1314	1296	0.9	-0.1	1.1	1.0	0.0	1.0	1.3	0.4	0.7		
GYPSY10	Gypsy	71	1294	168	1453	1670	235	1468	1482	1.3	0.4	1.3	1.4	0.5	1.4	1.0	0.0	1.0		
GTWIN	Gypsy	70	1906	412	1571	1220	566	1563	606	0.6	-0.6	1.6	1.4	0.5	0.7	1.0	0.0	1.0		
S_DM	Mariner/Tc1	69	1637	1461	1382	1571	1429	1329	1604	1.0	-0.1	1.0	1.0	0.0	1.0	1.0	-0.1	1.0		
GYPSY15	Gypsy	68	1021	190	1386	2326	1515	1699	1673	2.3	1.2	2.3	8.0	3.0	8.0	1.2	0.3	1.2		
GYPSY16	Gypsy	67	407	249	379	316	310	310	241	2.1	2.0	2.0	1.0	0.0	1.0	1.0	0.0	1.0		
INVADER2	Gypsy	66	1805	1625	1519	1549	1411	1249	1679	0.0	-0.2	1.2	0.9	-0.2	1.2	0.8	-0.3	1.2		
QUASIMODO2 + LTR	Gypsy	65	1105	1354	1544	2266	2696	1597	1682	2.0	1.0	2.0	2.0	1.0	2.0	1.0	0.0	1.0		
DNAREP1_DM	He100	64	1722	1986	1633	1675	1794	1553	1699	1.0	0.0	1.0	0.9	-0.1	1.1	1.0	-0.1	1.1		
IDF1N	Gypsy	63	1701	926	1673	2093	1502	1492	1897	1.2	0.3	1.2	1.6	0.7	1.6	0.9	-0.2	0.9		
TRANSIB2	Transib	62	1812	2047	1545	2136	1878	2053	1974	1.2	0.2	1.2	0.9	-0.1	0.9	1.3	0.4	1.3		
DIVER3	POGO	61	1994	1940	1462	2041	1669	1624	2016	1.0	0.0	1.0	0.9	-0.2	0.9	1.1	0.2	1.1		
DRB_DM	hAT	60	1576	1342	2709	2455	2505	2707	2045	0.7	-0.6	1.6	2.2	1.1	2.2	1.0	0.0	1.0		
GYPSY17	Gypsy	59	2059	1994	2447	3992	3005	2447	2144	1.4	0.5	1.4	2.0	1.0	2.0	1.0	0.0	1.0		
GYPSY18	Gypsy	58	2059	1994	2447	3992	3005	2447	2144	1.4	0.5	1.4	2.0	1.0	2.0	1.0	0.0	1.0		
GYPSY19	Gypsy	57	364	126	1077	3992	4337	3483	2178	11.0	3.5	11.0	34.3	5.1	34.3	3.2	1.7	3.2		
TIRANT	TIRANT	56	364	126	1077	3992	4337	3483	2178	11.0	3.5	11.0	34.3	5.1	34.3	3.2	1.7	3.2		
GYPSY20	Gypsy	55	2976	1566	2583	1323	1019	2758	3506	0.2	-2.1	4.3	0.2	-2.4	5.2	1.1	0.1	0.9		
GYPSY21	Gypsy	54	3915	2398	2398	7215	1203	2398	3506	0.2	-2.5	5.1	0.2	-2.5	5.7	1.1	0.0	0.9		
GYPSY22	Gypsy	53	1740	1885	2245	3716	3007	2245	2799	2.0	1.0	2.0	1.6	0.7	1.6	1.0	0.0	1.0		
GYPSY23	Gypsy	52	3814	2685	2114	2127	1792	2111	2622	0.7	-0.6	1.5	0.7	-0.5	1.5	1.0	0.0	1.0		
GYPSY24	Gypsy	51	3124	2709	2505	2505	2505	2705	2705	0.8	-0.4	1.4	0.5	-0.5	1.4	0.9	-0.1	1.4		
COPA_DM	Copia	50	1882	1885	2245	3716	3007	2245	2799	2.0	1.0	2.0	1.6	0.7	1.6	1.0	0.0	1.0		
GYPSY25	Gypsy	49	2742	1487	2307	2919	2051	2047	2831	1.1	0.1	1.1	1.4	0.5	1.4	0.9	-0.1	0.9		
GYPSY26	Gypsy	48	1791	2196	2238	3885	4257	2151	2838	2.2	1.1	2.2	1.9	1.0	1.9	1.0	-0.1	1.0		
GYPSY27	Gypsy	47	2706	1120	3293	3744	2120	3680	3225	1.4	0.5	1.4	1.9	0.9	1.9	1.1	0.2	1.1		
GYPSY28	Gypsy	46	3264	3908	3221	3302	3604	4766	4786	0.9	-0.2	1.1	0.8	-0.4	1.3	1.2	0.2	0.9		
BLASTOPIA	Gypsy	45	4916	5020	3022	1694	1492	2785	3305	0.3	-1.8	3.5	0.2	-2.3	4.9	0.9	-0.2	1.1		
GYPSY29	Gypsy	44	3070	3070	2306	1811	3263	5137	0.3	-1.8	3.5	0.2	-2.3	4.9	0.9	-0.2	1.1			
TART	Gypsy	43	5060	5181	4580	8556	8556	6289	7653	0.6	-0.5	1.6	0.5	-0.5	1.6	1.3	0.0	1.0		
LINE11_DM	Jockey	42	5627	5427	4514	6077	7301	5427	5132	1.2	0.2	1.2	1.4	0.5	1.4	1.3	0.1	1.1		
GYPSY30	Gypsy	41	5467	5467	4412	4696	5331	0.9	-0.2	1.1	1.4	0.5	0.7	1.0	0.9	-0.1	1.1			
GYPSY31	Gypsy	40	4444	4037	4431	4818	5281	4408	4629	1.1	0.1	1.1	1.3	0.4	1.3	1.1	0.1	1.0		
TAHRE	Jockey	39	5704	5704	4283	4876	5128	4721	5896	5415	0.9	-0.2								

Table S3. Analysis of piRNAs mapping to I-element fragments

#chr	chrom_start	chrom_end	chrom_orientation	length	contained genome unique 25mers [%]	start_in_repeat	end_in_repeat	substitutions [nt/kb]	deletions [nt/kb]	insertions [nt/kb]	wk parents all mappers [RAW DATA]	wk parents genome unique [RAW DATA]	wi118 parents all mappers [RAW DATA]	wi118 parents genome unique [RAW DATA]	wk parents all mappers [normalized to 1Mio small RNAs]	wi118 parents genome unique [normalized to 1Mio small RNAs]	wk parents all mappers [normalized to 1Mio small RNAs/bp]	wi118 parents genome unique [normalized to 1Mio small RNAs/bp]	wk parents density [unique piRNAs/bp]	wi118 parents density [unique piRNAs/bp]	wk parents density [normalized to 1Mio small RNAs]	wi118 parents density [normalized to 1Mio small RNAs]			
chr2L	21395008	21395161	-	156	52.6	2008	2158	101	0	1	10	0	0.3	0.3	2.4	0.0	0.002	0.000	0.000	0.000	0.000	0.000			
chr2L	21395470	21395730	-	307	11.3	1700	2007	55	3	0	1	61	0	2.0	0.0	14.7	0.0	0.000	0.000	0.000	0.000	0.000	0.000		
chr2L	21413443	21413531	+	207	2.9	1800	2007	72	5	0	1	19	0	0.3	0.3	4.6	0.0	0.000	0.000	0.000	0.000	0.000	0.000		
chr2L	21413609	21413681	+	772	43.7	2004	2782	10	1	1	2	366	1	3.4	0.3	88.4	0.2	0.001	0.000	0.000	0.000	0.000	0.000		
chr2L	21414380	21415983	+	1613	35.8	3286	3525	66	1	4	42	1	1449	11.7	0.3	350.0	1.7	0.000	0.001	0.000	0.000	0.000	0.000		
chr2L	21415985	21416185	+	200	42.9	5265	5461	45	10	25	0	0	33	0	0.0	0.0	8.0	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2L	22254584	22254732	-	148	100.0	2101	2257	274	74	14	0	0	0	0.0	0.0	0.0	0.0	0.000	0.000	0.000	0.000	0.000	0.000		
chr2L	22321247	22321803	-	556	31.5	3555	3745	190	68	5	1	0	4	1	0.3	0.0	1.0	0.2	0.000	0.000	0.000	0.000	0.000	0.000	
chr2L	22699123	22701173	+	2053	33.3	98	2220	61	40	6	65	0	1113	13	18.2	0.0	268.8	3.1	0.000	0.002	0.000	0.000	0.000	0.000	
chr2L	22719313	22719369	-	56	0.0	5145	5200	85	0	0	7	0	0	4	0	2.0	0.0	1.0	0.0	0.000	0.000	0.000	0.000	0.000	0.000
chr2L	22721058	22721201	-	143	0.0	4999	5144	77	42	0	5	0	127	0	1.4	0.0	30.7	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2L	22721199	22721438	-	239	0.0	4172	4411	161	17	13	8	0	85	0	2.2	0.0	20.5	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2L	22730019	22730071	-	52	0.0	5145	5201	93	93	0	3	0	2	0	0.8	0.0	0.5	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2L	22731762	22732133	-	371	24.4	4994	5144	137	52	20	9	0	155	14	2.5	0.0	37.4	3.4	0.000	0.009	0.000	0.000	0.000	0.000	
chr2L	22746550	22746665	+	115	84.8	5059	5182	122	78	0	1	1	2	2	0.3	0.3	0.5	0.5	0.002	0.004	0.000	0.000	0.000	0.000	
chr2L	22757695	22758075	-	380	7.0	4172	4450	136	33	24	13	0	212	3	3.6	0.0	51.2	0.7	0.000	0.002	0.000	0.000	0.000	0.000	
chr2L	22768340	22768711	+	378	0.0	4172	4450	136	33	25	10	0	178	0	2.8	0.0	43.0	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2L	22770385	22770441	+	56	0.0	5145	5199	103	0	14	0	0	0	2	0	0.0	0.0	0.5	0.0	0.000	0.000	0.000	0.000	0.000	0.000
chr2L	22775458	22775836	-	378	0.0	4172	4450	136	36	25	10	0	178	0	2.8	0.0	43.0	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2L	22777503	22777559	-	56	0.0	5145	5199	103	0	14	0	0	0	2	0	0.0	0.0	0.5	0.0	0.000	0.000	0.000	0.000	0.000	0.000
chr2L	22916456	22916785	-	329	100.0	1588	1918	175	43	27	0	0	0	0	0.0	0.0	0.0	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2RHet	10160	10419	+	259	50.8	5213	5464	72	4	31	0	0	0	0	0	0.0	0.0	0.0	0.0	0.000	0.000	0.000	0.000	0.000	0.000
chr2RHet	12359	17644	-	5285	28.0	99	5464	61	18	3	155	2	3104	21	43.3	0.6	749.8	5.1	0.000	0.001	0.000	0.000	0.000	0.000	
chr2RHet	142423	117124	-	2881	22.5	83	2983	59	14	7	97	0	1397	6	27.1	0.0	337.4	1.4	0.000	0.001	0.000	0.000	0.000	0.000	
chr2RHet	117794	118604	-	810	18.3	4680	5077	64	12	1	13	0	500	2	3.6	0.0	120.8	0.5	0.000	0.001	0.000	0.000	0.000	0.000	
chr2RHet	147058	147258	-	463	73.6	471	5464	123	19	4	0	0	21	0	0.0	0.0	0.5	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2RHet	545802	545809	-	707	30.9	4758	5459	59	3	10	15	0	202	5	4.2	0.0	48.8	1.2	0.001	0.002	0.000	0.000	0.000	0.000	
chr2RHet	546513	547744	-	1231	44.4	3333	3567	57	2	1	31	0	637	28	8.7	0.0	153.9	5.6	0.000	0.005	0.000	0.000	0.000	0.000	
chr2RHet	547738	547983	-	245	51.8	2237	2516	53	143	0	4	0	167	12	1.1	0.0	40.3	2.9	0.000	0.012	0.000	0.000	0.000	0.000	
chr2RHet	547994	548593	-	602	50.8	981	1576	66	2	12	10	0	245	12	2.8	0.0	59.2	2.9	0.000	0.005	0.000	0.000	0.000	0.000	
chr2RHet	548592	548923	-	331	59.1	132	463	63	3	0	1	0	113	2	0.3	0.0	27.3	0.5	0.000	0.001	0.000	0.000	0.000	0.000	
chr2RHet	752524	752911	-	767	49.1	116	902	53	26	0	15	1	302	10	4.2	0.3	72.9	2.4	0.000	0.003	0.000	0.000	0.000	0.000	
chr2RHet	753287	753362	-	75	94.2	1181	1255	114	13	67	0	0	15	7	0.0	0.0	3.6	1.7	0.000	0.023	0.000	0.000	0.000	0.000	
chr2RHet	753338	753867	-	529	36.0	1373	1911	60	38	19	13	0	259	13	3.6	0.0	62.6	3.1	0.000	0.006	0.000	0.000	0.000	0.000	
chr2RHet	754107	755339	-	1532	45.3	1907	3436	55	6	7	41	1	1368	27	11.5	0.3	330.4	6.5	0.000	0.004	0.000	0.000	0.000	0.000	
chr2RHet	826511	826907	-	3096	25.1	2327	5464	67	14	1	87	2	2736	19	24.3	0.6	660.9	4.6	0.000	0.001	0.000	0.000	0.000	0.000	
chr2RHet	889676	890376	-	700	36.8	431	1130	41	26	26	21	1	393	16	5.9	0.3	94.9	3.9	0.000	0.006	0.000	0.000	0.000	0.000	
chr2RHet	890375	890720	-	345	38.5	1447	1785	66	14	32	30	5	114	1	8.4	1.4	27.5	0.2	0.004	0.001	0.000	0.000	0.000	0.000	
chr2RHet	899753	901823	-	2070	36.2	1772	3895	63	28	2	59	1	1808	28	16.5	0.3	436.7	6.8	0.000	0.003	0.000	0.000	0.000	0.000	
chr2RHet	913879	915374	-	1495	38.0	3888	5459	64	56	3	38	0	1114	25	10.6	0.0	269.1	6.0	0.000	0.004	0.000	0.000	0.000	0.000	
chr2RHet	960433	961499	-	1065	0.0	108	1186	50	45	0	50	0	780	0	14.0	0.0	188.4	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2RHet	961684	962244	-	1040	9.4	108	1186	50	45	0	50	0	710	0	14.0	0.6	171.5	0.0	0.001	0.000	0.000	0.000	0.000	0.000	
chr2RHet	977766	978823	-	1062	1.8	108	1186	44	24	0	50	0	847	0	14.0	0.0	204.6	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2RHet	990855	991041	-	185	54.3	2127	2317	151	32	0	3	2	11	1	0.8	0.6	2.7	0.2	0.003	0.001	0.000	0.000	0.000	0.000	
chr2RHet	12565239	12565116	-	187	59.1	2127	2319	160	32	0	4	3	20	9	1.1	0.8	4.8	2.2	0.004	0.012	0.000	0.000	0.000	0.000	
chr2RHet	12619249	12620051	-	1445	37.0	4400	4556	79	8	9	51	0	179	42	14.2	0.6	197.8	6.1	0.000	0.007	0.000	0.000	0.000	0.000	
chr2RHet	12659249	12659361	-	2365	33.3	1497	3868	63	18	9	99	19	2112	23	27.7	5.3	51.1	5.17	0.002	0.022	0.000	0.000	0.000	0.000	
chr2RHet	12810409	12810493	-	226	0.0	208	2549	568	68	0	4	0	1495	20	21.5	0.0	358.7	0.0	0.000	0.000	0.000	0.000	0.000	0.000	
chr2RHet	12821314	12821560	-	1846	0.0	88	1936	59	10	0	62	0	1123	17</											

chr3Het	822600	823762	-	1162	64.2	3553	4726	93	24	14	12	0	386	1	3.4	0.0	93.2	0.2	0.000	0.000
chr3Het	823782	824432	-	650	83.1	2258	2920	91	20	0	10	1	82	1	2.8	0.3	19.8	0.2	0.000	0.000
chr3Het	824425	824590	-	165	62.7	1473	1937	126	6	6	1	0	2	0	0.3	0.5	0.0	0.0	0.000	0.000
chr3Het	824590	838811	-	1630	54.9	1024	1734	70	24	20	49	1	506	8	137	0.3	122.2	1.9	0.000	0.001
chr3Het	1028801	1040771	-	1957	26.5	2056	4025	59	38	1	48	0	1664	14	134.4	0.0	401.9	3.4	0.000	0.002
chr3Het	1038807	1040748	-	1941	30.5	89	2010	62	9	19	69	0	893	18	19.3	0.0	215.7	2.4	0.000	0.001
chr3Het	1120350	1120863	-	513	5.1	1380	1930	90	82	8	14	0	55	0	3.9	0.0	13.3	0.0	0.000	0.000
chr3Het	1120860	1121812	-	952	55.7	98	1146	114	104	3	2	0	90	0	0.6	0.0	21.7	0.0	0.000	0.000
chr3Het	1123072	1124056	-	984	18.5	4372	5473	132	123	3	13	0	183	0	3.6	0.0	44.2	0.0	0.000	0.000
chr3Het	1124063	1124549	-	486	68.5	3462	3965	178	43	6	7	2	84	0	2.0	0.6	20.3	0.0	0.001	0.000
chr3Het	1125263	1125776	-	513	0.0	1380	1930	88	82	8	14	0	116	0	3.9	0.0	28.0	0.0	0.000	0.000
chr3Het	1125773	1126745	-	972	2.0	99	1146	70	80	2	6	0	187	0	1.7	0.0	45.2	0.0	0.000	0.000
chr3Het	1128010	1128995	-	985	15.6	4371	5473	102	123	3	24	0	677	4	6.7	0.0	163.5	1.0	0.000	0.001
chr3Het	1129014	1129489	-	475	42.9	3462	3950	95	30	0	5	0	111	2	1.4	0.0	26.8	0.5	0.000	0.001
chr3Het	1543578	1544664	+	1086	39.3	4340	5470	68	47	6	22	3	458	23	6.1	0.8	110.6	5.6	0.001	0.005
chr3R	2151185	2151240	-	55	100.0	2600	2661	164	18	0	1	1	0	0	0.3	0.0	0.0	0.0	0.005	0.000
chr3R	2291375	2292115	-	740	83.7	4684	5470	101	69	5	2	1	83	21	0.6	0.3	20.0	5.1	0.000	0.007
chr3R	2292124	2292176	-	52	100.0	4074	4126	115	19	0	0	0	10	10	0.0	0.0	2.4	2.4	0.000	0.046
chr3R	2292470	2292779	-	309	75.9	3663	3978	126	23	0	1	0	6	0	0.3	0.0	1.4	0.0	0.000	0.000
chr3R	2300381	2300485	-	104	84.0	3561	3673	135	10	0	0	0	3	3	0.0	0.0	0.7	0.7	0.000	0.007
chr3R	2431304	2432572	-	1272	32.2	1744	3102	81	94	29	20	1	772	1	5.6	0.3	186.5	0.2	0.000	0.000
chr3R	2432863	2434528	-	1665	14.3	108	1751	60	3	11	129	11	831	3	36.0	3.1	200.7	0.7	0.002	0.000
chr3R	2485075	2487837	+	2762	19.9	103	3007	65	65	13	131	3	1333	40	36.8	0.8	322.0	9.7	0.000	0.003
chr3R	1200442	1200540	-	98	100.0	5366	5471	194	82	0	0	0	0	0	0.0	0.0	0.0	0.0	0.000	0.000
chr3R	9201524	9201574	+	324	95.7	2859	3253	121	12	80	0	0	6	0	0.0	0.0	1.4	0.0	0.000	0.000
chr4	164375	165959	+	1591	68.5	2454	2849	83	64	0	53	22	644	48	14.8	0.0	151.6	11.6	0.004	0.007
chr4	167120	1685558	+	1438	57.0	3974	5464	85	52	16	22	1	844	26	6.1	0.3	203.9	6.3	0.000	0.004
chrU	173777	173823	-	1905	18.3	3563	5473	61	5	2	35	0	830	3	9.8	0.0	200.5	8.5	0.000	0.004
chrU	89286	89623	-	337	35.7	2841	3176	65	0	3	5	0	503	6	1.4	0.0	121.5	1.4	0.000	0.004
chrU	89613	90667	-	1054	36.0	1320	2451	55	84	10	23	0	448	11	6.4	0.0	108.2	2.7	0.000	0.003
chrU	99966	100221	-	255	7.3	1074	1330	67	0	16	1	66	7	4.5	0.3	15.9	1.7	0.001	0.007	
chrU	100222	101064	-	842	33.7	104	965	58	32	4	25	3	443	17	7.0	0.8	107.0	4.1	0.001	0.005
chrU	220679	221409	-	730	62.2	1354	2067	86	10	31	1	0	249	18	0.3	0.0	60.1	4.3	0.000	0.006
chrU	221426	222141	-	715	69.5	108	818	86	8	3	14	2	210	11	3.9	0.6	50.7	2.7	0.001	0.004
chrU	623852	627395	-	3543	52.1	1722	5464	65	61	5	81	5	2469	137	22.6	1.4	596.4	33.1	0.000	0.009
chrU	627406	628428	-	1022	71.1	611	1647	70	28	14	28	3	380	23	7.8	0.8	91.8	5.6	0.001	0.005
chrU	628454	628652	-	198	63.4	100	297	76	0	0	0	0	38	0	0.0	0.0	9.2	0.0	0.000	0.000
chrU	1188383	1188493	+	110	100.0	3363	3472	318	0	0	0	2	0	0.0	0.0	0.5	0.5	0.000	0.004	
chrU	1230155	1230929	-	774	29.0	4696	5464	60	3	9	17	0	329	49	4.7	0.0	79.5	11.8	0.000	0.015
chrU	1233661	1233715	-	54	100.0	216	272	130	56	0	0	0	0	0.0	0.0	0.0	0.0	0.0	0.000	
chrU	1233716	1238702	+	4986	14.9	274	5433	61	38	3	157	4	4192	13	43.9	0.0	1012.6	3.1	0.001	0.001
chrU	1371335	1376337	+	5002	11.9	318	5482	62	35	3	147	4	3915	28	41.1	1.1	945.7	6.8	0.000	0.001
chrU	1772742	1775004	-	2266	0.0	3225	5480	68	0	4	77	0	1485	0	21.5	0.0	358.7	0.0	0.000	0.000
chrU	1775007	1776853	-	1846	0.0	88	1936	59	10	9	62	0	1123	0	17.3	0.0	271.3	0.0	0.000	0.000
chrU	2203633	2206743	+	3111	35.7	99	3236	62	13	5	14	6	2571	109	31.8	1.7	621.0	26.3	0.001	0.008
chrU	2206743	2208743	+	1990	44.4	3433	5461	73	20	1	34	0	989	29	9.5	0.0	238.9	7.0	0.000	0.004
chrU	2306982	2308105	+	1123	42.4	49	3881	59	142	0	54	4	605	21	15.1	1.1	146.1	5.1	0.000	0.005
chrU	2308102	230812	+	801	25.9	2867	3469	60	16	0	34	2	1100	35	9.5	0.6	265.7	8.5	0.001	0.010
chrU	2309436	2310235	+	815	21.3	4632	5482	39	45	1	13	0	515	36	3.6	0.0	124.4	4.1	0.000	0.005
chrU	23994977	2995334	-	407	35.2	3503	3892	266	61	103	3	90	5	0	0.8	0.0	1.2	0.0	0.000	0.000
chrU	3235091	3238292	-	3201	31.1	2558	4746	69	7	1	90	3	2208	25	25.1	0.8	533.3	6.0	0.000	0.002
chrU	3560090	3560779	-	689	0.0	4300	4989	71	1	0	24	0	368	0	6.7	0.0	88.9	0.0	0.000	0.000
chrU	3567519	3569700	-	2181	21.3	2793	4989	69	9	2	81	1	1856	19	22.6	0.3	448.3	4.6	0.000	0.002
chrU	5494351	5496276	+	1925	10.8	56	2022	93	38	16	25	0	559	5	7.0	0.0	135.0	1.2	0.000	0.001
chrU	5496272	5497989	-	1717	1.5	1829	3735	86	122	11	30	0	682	1	8.4	0.0	164.7	0.2	0.000	0.000
chrU	5497988	5498439	+	451	0.0	4120	4578	89	18	0	12	0	109	0	3.4	0.0	26.3	0.0	0.000	0.000
chrU	5498783	5498940	+	157	0.0	4570	4729	70	19	0	2	0	23	0	0.6	0.0	5.6	0.0	0.000	0.000
chrU	5498945	5499371	+	426	12.2	4976	5406	83	16	5	2	0	41	0	0.6	0.0	9.9	0.0	0.000	0.000
chrU	6540925	6541600	-	681	18.7	1380	2136	78	118	7	14	0	147	0	3.9	0.0	35.5	0.0	0.000	0.000
chrU	6541603	6542575	-	972	2.6	99	1146	71	80	2	6	0	187	0	1.7	0.0	45.2	0.0	0.000	0.000
chrU	9614059	9614255	-	196	24.3	991	1186	61	0	0	11	0	73	1	3.1	0.0	17.6	0.2	0.000	0.001
chrXhet	33738	34393	+	655	4.0	2994	3660	310	69	50	0	0	3	0	0.0	0.0	0.7	0.0	0.000	0.000
chrXhet	42639	43294	+	655	4.0	2994	3660	309	69	50	0	0	3	0	0.0	0.0	0.7	0.0</		

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